



Heat stress and yield stability of wheat genotypes under different sowing dates across agro-ecosystems in India

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ABSTRACT

Among the most significant impacts of climate change is the potential increase of food insecurity. The predicted impact of temperature rise due to climate change on the crop production and productivity can be mediated through different crop management adaptations such as shifted sowing dates. We investigated the effects of sowing dates on yield stability of wheat across agro-ecosystems and years using multi-environment trials. The objectives of the study were as follows: (i) to evaluate the genotype \times environment \times management ($G \times E \times M$) for wheat genotypes, (ii) to predict yield performance and identify high stable wheat genotypes in different management practices, and (iii) to make genotype-specific management and high performing genotype recommendations within and across agro-ecological regions. A diverse set of twenty-one genotypes was evaluated over three years (2012–2014) under ten levels of crop management practices (ten different dates of sowing: D01–D10) across three agro-ecological regions (BR, MP and PB) of India in replicated trials. Data were analyzed with SAS $G \times E$ and RG $G \times E$ programs using SAS and R programming languages, respectively. Results revealed that the impact of shifted sowing dates on yield stability was unevenly spread across management practices. Across locations, the genotype ‘CSW 18’ (G03), ‘DPW 621-50’ (G05), ‘BAZ’ (G01) were the best performer and high stable in early, normal and later sowing dates, respectively. Across and within an individual location(s), the pattern of predicted yield suggests that the low performing genotypes during early sowing dates tend to become high performer during late sowing dates. Similarly, high predictive yield and high stable genotypes from early planting tend to have variable predicted yield with low stability during normal and late sowing dates for across and within an individual location(s). Low predictive yield and low stable genotypes had disease resistant genes and, thus, can be served as parent for future breeding, where trait value low is desired.

Abbreviations: AEC, average environment coordinate; ANOVA, analysis of variance; BLUP, best linear unbiased predictor; BR, Pusa Bihar; DOS, date of sowing; D01, first DOS (Oct 15 in the year 2012, 2013 and 2014); D02, second DOS (DOS1 + 7 days); D03, third DOS (DOS2 + 7 days); D04, fourth DOS (DOS3 + 7 days); D05, fifth DOS (DOS4 + 7 days); D06, sixth DOS (DOS5 + 7 days); D07, seventh DOS (DOS6 + 7 days); D08, eighth DOS (DOS7 + 7 days); D09, ninth DOS (DOS8 + 7 days); D10, tenth DOS (DOS9 + 7 days); GGE, genotype main effects plus genotypic \times environment interaction effect; GGL, genotype main effects plus genotypic \times location interaction effect; $G \times E$, genotype \times environment interaction; $G \times M \times E$ or $G \times M \times L \times Y$, genotype \times management \times environment interaction or genotype \times management \times location \times year interaction; G, genotype; G01 or 1, BAZ; G02 or 2, CSW 16; G03 or 3, CSW 18; G04 or 4, DBW 17; G05 or 5, DBW 88; G06 or 6, DPW 621-50; G07 or 7, GW 273; G08 or 8, GW 366; G09 or 9, GW 322; G10 or 10, HD 2824; G11 or 11, HD 2687; G12 or 12, HD 2733; G13 or 13, HD 2932; G14 or 14, HD 2967; G15 or 15, HI 1563; G16 or 16, JW 3288; G17 or 17, K 307; G18 or 18, MPO 1215; G19 or 19, Munal; G20 or 20, PBW 343; G21 or 21, PBW 550; HYHS, high yield and high stable; HYLs, high yield and low stable; L, location; LYHS, low yield and high stable; LYLS, low yield and low stable; M, management; MET, multi-environment trial; MP, Jabalpur, Madhya Pradesh; MYHS, medium yield and high stable; MYLS, medium yield and low stable; PB, Ludhiana, Punjab; PC, principal component; RG $G \times E$, R language program for the analysis of genotype stability and location value; REML, restricted maximum likelihood; SAS $G \times E$, SAS program for the analysis of genotype stability and location value; SVP, singular value partitioning; Y, year

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1. Introduction

Climate change threatens to exacerbate existing threats to food security and livelihoods due to a combination of factors that include the increasing frequency and intensity of climate hazards, diminishing agricultural yields and reduced production in vulnerable regions, rising health and sanitation risks, increasing water scarcity, and intensifying conflicts over scarce resources, which would lead to new humanitarian crises as well as increasing displacement (IPCC, 2007). Understanding the specific impacts of climate change on food security is challenging because vulnerabilities are unevenly spread across the world. Even remote changes in climatic conditions can affect food security elsewhere. For examples, temperature changes affect the timing of runoff in Ganges catchments, causing an increase in peak flow during the monsoon period, but dry season river-flow is still very low (Stern, 2007). One of the most significant long-term climate change is temperature rise. Global average temperature is expected to rise as a result of climate change, and the spatial pattern of this rise is such that all areas will see an increase in temperature. By the 2050s the global average temperature is projected to have risen between 2 and 4 °C above the pre-industrial climate. Empirical evidence suggests that increases in temperature in the period 1980–2008 have already resulted in average global maize and wheat yield reductions of 3.8% and 5.5% respectively, compared to a non-climate scenario (Lobell et al., 2011). Yield is a complex quantitative trait and greatly influenced by external environment, which results in scale or rank shift in its performance (Dia, 2012; Dia et al., 2016a). This relative shift of genotype performance from one environment (location \times year combination) to another is known as genotype \times environment interaction ($G \times E$) (Dia et al., 2012a; Dia et al., 2012b).

Increases in local temperatures can generate devastating agricultural losses, and can be critical if they coincide with key stages of crop development (Wollenweber et al., 2003). The yields of many cereal crops can be drastically reduced by temperatures above 32 °C during the flowering stage: for instance, rice grain sterility occurs in temperatures in the mid–30s (Porter and Gawith, 1999; Wheeler et al., 2000; VaraPrasad et al., 2003; Hatfield et al., 2011). Empirical studies using historical crop-trial data have predicted that adverse impact of heat stress on crop yield can be mitigated by shifting sowing dates (Dhillon and Ortiz-Monasterio, 1993). Substantial studies have been conducted to identify high yielding and consistent performing genotypes (also known as stable genotypes). However, most of the high stable genotypes are less predictable across shifted sowing dates (crop management practices) since plant breeders often perform analysis of two-way data (genotype \times site or $G \times E$) for several consecutive years to detect stable genotypes without taking crop management practices into account (Dia, 2005; Dia et al., 2009; Gathala et al., 2011; Jat et al., 2009; Jat et al., 2013; Sapkota et al., 2017; Weindorf et al., 2008a; Weindorf et al., 2008b). Approximately one-sixth of the world's population currently lives in glacier-fed river basins where temperatures are projected to increase, particularly in areas such as the Indo-Gangetic Plain; these elevated temperature pressures will result in greater stress on crop yield and stability (Stern, 2007). Although little research has been carried out on the impacts of heat stress on crop yield, it is important to assess the potential effects, particularly in the context of yield stability. In this paper, we propose to identify high yielding and high stable wheat genotypes across Indo-Gangetic Plain (environments) and over ten different sowing dates (crop management practices).

The impenetrable interaction of a crop bio-system with the soil, the atmosphere, and the environment that a plant lives in introduces challenges when making breeding decisions because it complicates the demonstration of superiority of any genotype across environments. Genotype \times environment interaction may result in low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This reduction leads to bias in the estimation of heritability and in the prediction of genetic advance (Comstock and Moll,

1963; Alghamdi, 2004; Kumar et al., 2013a). Several strategies have been proposed to deal with $G \times E$, and the most powerful strategy is to exploit $G \times E$ either to develop locally adapted material or to use $G \times E$ to better characterize the genotypes (DeLacy et al., 1996; Mathews et al., 2008). Genotype \times environment interaction can be characterized using statistical methods ranging from univariate to multivariate models. The univariate models include regression slope, deviation from regression, environmental variance, and Kang's yield-stability; multivariate models include genotype main effects plus genotype by environment interaction (GGE) biplot, and additive main effects and multiplicative interaction (AMMI) (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Shukla, 1972; Yan, 2001; Kang, 1993; Yan and Kang, 2003; Gauch, 2006). Multivariate models could be graphically represented through biplots where genotypes and environments are plotted in a single graph. Recently, hierarchical Bayesian and mixed models were introduced to model heterogeneous variance among environments and different correlation structures among environments (Jat and Serre, 2016; Jarquín et al., 2016; Li et al., 2010; Malosetti et al., 2004; Mathews et al., 2008). Mixed models allow more flexibility to model unbalanced data using restricted maximum likelihood estimates (REML). Each statistical method reflects different aspects of the $G \times E$, and no single method adequately explains genotype performance across environments (Dia et al., 2016a). Stability statistics are best used in combination with trait performance (mean or BLUP: Best Linear Unbiased Predictor is an estimate of random effect) and have successfully been used in plant breeding.

In this study, we were interested in understanding differential sensitivity of certain wheat genotypes to different agro-ecological environments in India under shifted sowing dates for enhancing the selection of superior and stable genotypes. The objectives of the study were as follows: (i) to evaluate the genotype \times environment \times management interaction ($G \times E \times M$) for wheat genotypes, (ii) to predict yield performance and identify high stable wheat genotypes in different management practices, and (iii) to make genotype-specific management and high performing genotype recommendations within and across agro-ecological regions.

2. Materials and methods

2.1. Germplasm, location and management

Twenty-one genotypes of wheat were evaluated across three years (2012–2014) and three locations ranging from western to eastern Indo-Gangetic plains under ten different dates of sowing (management practices). Locations were chosen to represent the major wheat growing agro-ecological conditions for major wheat production regions in India: Pusa (25° 57' 08" N; 85° 40' 13" E), Bihar (BR), Jabalpur (23° 10' 7.6" N; 79° 55' 55" E), Madhya Pradesh (MP), and Ludhiana (30° 59' 28" N; 75° 44' 11" E), Punjab (PB) (Supplemental Figs. 1 and 2). The soils of the experimental plots at three locations, PB, MP and BR, were sandy loam, clay loam and silty loam, respectively. Twenty-one genotypes were semi-dwarf spring wheat chosen to represent new vs. old release; stress resistant vs. susceptible; rust resistant vs. susceptible; eastern vs. northern adapted; tall vs. short stature; early vs. late maturity; low vs. high yield; and varied 1000 kernel weight, protein content, spikelets ear^{-1} and seeds spike^{-1} . These genotypes are advanced breeding lines or officially released cultivars. Here after the word 'genotype' is used to indicate cultivar, cultivar, variety or genotype. Genotypes were considered to be random and representative samples of a wide range of genetic and phenotypic diversity in the wheat germplasm population (Table 1). Wheat genotypes were evaluated at ten levels of crop management: date of sowing (D01 to D10). Ten dates of sowing were evenly spaced at 7 days apart with D01 (first date of sowing) and D10 (last date of sowing) scheduled for October 15 and December 17, respectively, for all three years (2012–2014). In Indo-Gangetic plains, the wheat sowing times are broadly classified into three categories: early (October),

Table 1
The 21 wheat genotypes tested with pedigree, phenotype and genotypic information.
Source: Wheat Atlas – <http://wheatatlas.org/>.

ID	Genotype ^a	Year of release	Phenotype				Genotype/genes				
			Pedigree ^d	Maturity ^e	Height ^f	YP ^d (tha ⁻¹)	TKW ^j (g)	Grain ^h	Type ^b	Resistant to Stem- Yellow- Leaf- Rust Ug99 + Stress ^k	
G01	BAZ ^A	UT ^c	M	S	5.50	40.2	WB	B	Y - - Y + H	APR (Sr2 +)	
G02	CSW 16 ^A	PPVFRA ^c	L	M	7.00	44.0	BMHL	B	- Y Y - + -		
G03	CSW 18 ^A	2016	L	T	7.00	40.0	LH	B	- Y - - + -		
G04	DBW 17 ^p	2007	M	S	6.30	37.0	AMBHL	B	- Y Y N + H		ne1,ne2; Lr23Lr26+; Lr46; no-Lr34; Lr1,no-Lr10,no-Lr19,Lr26,no-Lr34(MM); Sr2,Sr31+; Yr9+; marker_Cre3_280,Cre5;
G05	DPW 621-50 ^A	2011	L	M	6.98	38.0	-	B	- Y Y - + -		
G06	DBW 88 ^p	2014	L	M	6.99	38.0	AHM	B	- Y Y - + VD		Lr10,Lr13+; Sr11+;
G07	GW 273 ^x	1998	M	M	5.02	42.8	AHM	B	- - - N+-		Glu-A1b,Glu-B1i,Glu-D1d;
G08	GW 322 ^M	2002	E	S	6.63	40.3	ASB	B	- - - N + D		Lr1,Lr10,Lr13; Lr13+; no-Lr34; Sr2,Sr11+; Yr2+; Glu-A1b,Glu-B1b,Glu-D1a; no-1RS;
G09	GW 366 ^x	2007	E	M	7.79	49.0	WB	B	Y - Y N + VD		ne1,ne2; Lr1,Lr23,Lr26,LrAPR1; Lr1,Lr23,Lr26; no-Lr34; Yr9; no-1RS;
G10	HD 2687 ^y	1999	M	M	5.12	35.2	AHM	B	- - - N+-		Lr1,no-Lr10,no-Lr19,no-Lr34(MM); Glu-A1b,B1d,D1a;
G11	HD 2733 ^B	2001	M	S	7.15	41.0	AHB	B	Y Y Y N + L		Ne1,ne2; Lr26,Lr34; Lr26; no-Lr34; Lr1,no-Lr10,no-Lr19,Lr26,no-Lr34(MM); Sr31+; Yr9,Yr18; T1BL1RS; Glu-A1b,B1d,D1d;
G12	HD 2824 ^B	2004	M	S	7.04	41.0	ASB	B	- - - N + L		Lr23,Lr26; no-Lr34; Lr1,no-Lr10,no-Lr19,Lr26,no-Lr34(MM); Sr31; Yr9; T1BL1RS;
G13	HD 2932 ^M	2007	-	-	4.30	-	-	B	- - - N+-		Lr13+; no-Lr34; Lr1,no-Lr10,no-Lr19,no-Lr26,no-Lr34(MM);
G14	HD 2967 ^A	2011	L	M	6.61	-	AMBHL	B	- Y Y -+-		
G15	HI 1563 ^B	2011	E	S	5.17	-	-	B	Y Y Y -+-		
G16	JW-3288 ^M	2011	M	S	4.39	44.0	-	B	Y - Y -+-		
G17	K 307 ^B	2007	M	M	6.51	39.1	-	B	- - - N+-		
G18	MPO 1215 ^M	2010	E	S	6.53	51.0	-	D	- - - N+-		
G19	Munal ^A	2011	L	T	7.00	40.2	-	B	- - - - + L		
G20	PBW 343 ^p	1996	M	M	6.10	41.6	ASB	B	N N - N+-		ne1,ne2; T1BL1RS; Lr26,Sr31,Yr9; Lr26,Lr34; Lr26; no-Lr34; Lr1,Lr10,no-Lr19,Lr26,no-Lr34(MM); Yr9,Yr18; Yr9,Yr27; cslV34a,no-Lm;
G21	PBW 550 ^p	2008	M	S	6.24	39.1	AMBHL	B	- Y Y N + VD		vrn1,vrn2,Vrn3; marker_Cre3_280,Cre5; Glu-A1a,B1a,D1d; Glu-A1a,B1c,D1d; Glu-A3c,B3k/b,D3b;
											ne1,ne2; Lr26,Lr34; no-Lr34; Lr1,no-Lr10,no-Lr19,Lr26,Lr34(MM);

^a ^A = tested in all location for 3 yrs; ^B = tested only in Bihar (BR) for 3 yrs; ^M = tested only in Madhya Pradesh (MP) for 3 yrs; ^P = tested only in Punjab (PB) for 3 yrs; ^X = tested only in MP for 1 yrs; ^Y = tested only in PB for 1 yrs. Genotypes 'BAZ', 'CSW 16' and 'CSW16' were missing in 2012 in MP in one replication. Similarly, 'CSW 18', and 'DPW 621-50' were missing from PB in 2014 in one replication.

^b Wheat type: Bread wheat (B); Durum wheat (D).

^c Under participatory trials and demonstration since 2011.

^d Yield potential.

^e Registered with PPVFRA (Protection of Plant Varieties and Farmers Right Authority, India).

^f Height: Short (S), < 90 cm; medium (M), 90–100 cm; Tall (T), > 100 cm.

^g Maturity: Early (E), < 120 days; medium (M), 120–140 days; late (L), > 140 days.

^h Grain characteristics: White and bold (WB); bold, medium hard and lustrous (BMHL); long and hard (LH); amber, medium bold, hard and lustrous (AMBHL); amber, hard and medium size (AHM); amber semi-hard and bold (ASB); amber hard and bold (AHB).

ⁱ ⁺ = backcross, ^{/'} = single cross, ^{/'/'} = double cross.

^j 1000 kernel weight.

^k ⁺ = Yes; [–] = No; [–] = No info; ^H = heat; ^{VD} = variable sowing dates; ^D = drought; ^L = lodging.

normal (November), and late (December) sowing. Thus, D01–D03, D04–D07, and D08–D10 falls into early, normal and late sowing categories, respectively. Zero tillage and other management practices correspond to the commercial wheat production in India were used (Choudhary et al., 2016; Jat et al., 2015). Recent studies on the effect of tillage practices on wheat productivity and cost-benefit ratio in Indo-Gangetic plains suggest the superiority of zero over conventional tillage (Jat et al., 2014; Mohanty et al., 2015; Parihar et al., 2016a, 2016b; Parihar et al., 2017; Yadav et al., 2016). In zero tillage, seeds were directly drilled without any preparatory tillage operations and in the presence of standing stubbles of rice residues (~15 cm) using 'Limit-Plot Planter' with inverted 'T' tyne openers (Kumar et al., 2013b; Singh et al., 2016a, 2016b). A standard seed rate (100 kg ha⁻¹), seeding depth (4 cm), fertilizer nutrient application (120 kg N, 60 kg P₂O₅ and 60 kg K₂O ha⁻¹), water management (irrigation at standard critical stages) was adopted for wheat crop management system (Aryal et al., 2016; Jat et al., 2014; Mohanty et al., 2015; Parihar et al., 2016a, 2016b; Parihar et al., 2017; Yadav et al., 2016).

2.2. Trials and data description

At each location, individual trials were established as a two-factor strip-plot (split-block) design with ten genotypes, three replications and ten-crop management practices (Mintenko et al., 2002). Out of the ten genotypes, six genotypes were tried at all three locations for three years, and the remaining four genotypes were location-specific and not necessarily duplicates. These four location-specific genotypes were evaluated at one or two location(s) for either one or all three years. Thus, total distinct genotypes were twenty-one (Table 1). Within the blocks, the genotypes were arranged in sub-blocks, and the two-crop managements in the other sub-blocks were arranged perpendicularly to the sub-blocks with the genotypes. The experimental unit (harvest plot) size was 1.6 m × 10 m.

In each location and year, the ten wheat genotypes were evaluated for grain yield (t ha⁻¹). Wheat grains were harvested using the guide of 15% moisture in grain, yellowing of spikelets and hard dough stage of grains (Jat et al., 2009). Data were missing at random from one replication, one location and one year for genotypes 'BAZ', 'CSW 16', 'CSW16', 'CSW 18', and 'DPW 621-50' (Table 1). We excluded three genotypes ('GW 273', 'GW 366' and 'HD 2687') that were tested for a time period shorter than three years and only in one location to provide a sufficient representative sample of years and location as random and fixed factors, respectively. As a result of this data preparation, we obtained a four-way genotype × management × location × year interaction (G × M × L × Y) dataset for the grain yield of eighteen wheat genotypes (Table 1). For across location analysis, management practices D01 and D10 were excluded. Thus, a set of six genotypes evaluated over 8 management practices in all locations were analyzed for across-location statistics. Likewise, for individual location BR and PB analysis we excluded management practices D01 and D10, respectively. Thus, a set of ten genotypes (six genotypes from all locations + four unique genotypes from each location) evaluated over 9 or 10 management practices were analyzed for individual location statistics (Table 1).

2.3. Data analysis and statistical methods

The unbalanced grain yield G × M × L × Y data were analyzed for genotype, environment, management, and genotype × environment × management interactions with the SASG × E (Dia et al., 2016a; Dia et al., 2016b; Dia et al., 2016c) and RG × E (Dia et al., 2017; Dia et al., 2016d) programs using SAS and R programming language, respectively, in two steps. During the first stage, we imputed the missing values using the mice() function of the mice (multivariate imputation by chained equations) package (Buuren and Groothuis-Oudshoorn, 2011) of R. Parameters maximum iteration 50, predictive mean matching (pmm) method and random generator seed value 500 were

used in the mice() function to generate five imputed datasets. Then, in the second stage, the five imputed datasets were combined across trials and years to obtain a balanced G × M × L × Y mean data for all statistical analyses.

Years and genotypes, and locations and managements were analyzed as random and fixed effects, respectively. Estimates and significance of random effects were computed using RG × E program. The random effect model was fit using the lmer() function of lme4 (linear mixed effects models) package (Bates et al., 2015). The *F* ratio (=MS_{between}/MS_{within}, where MS is mean square or variance estimate) and significance of fixed effects were computed using mixed() function of afex package (Singmann et al., 2015). The mixed() function computes type III such as *p*-values using the default method via the Kenward-Roger approximation for degrees of freedom. Similarly, the significance of random effects was computed using a likelihood ratio test to attain *p*-values. Likelihood is the probability of the data given a model. The logic of the likelihood ratio test is to compare the likelihood of two models with each other using restricted maximum likelihood (REML) methodology (Winter, 2013). Best linear unbiased predictor (BLUP) for genotypes were computed using ranef() function of lme4 package (Bates et al., 2015).

SASG × E provided R code that is ready to use in R statistical software (R Core Team, 2016) for the analysis of multivariate stability statistics (GGE biplot) (Dia et al., 2016c). GGE biplot analysis was computed using the 'GGEbiplotGUI' package (Frutos et al., 2014), with the support in the helper application 'RStudio' (RStudio, 2014) in R statistical software. GGE biplot analysis was used to visually assess the presence of genotype × environment interaction and rank genotype based on stability and mean in each management practice (Yan et al., 2000; Yan and Kang, 2003). For each management practice, input data of GGE biplot analysis consisted of genotype × environment matrix (2 × 2) of mean values.

Similar performing genotypes across and within locations and years were clustered using PROC VARCLUS of SAS v9.4 (SAS, 2016). The VARCLUS procedure used user-defined second eigenvalue cutoff and underlying algorithm called divisive clustering to split a given set of genotypes into two groups. Eigenvalues are the coefficients of principal component analysis. The value 1 of the second eigenvalue is a common choice for cut off because it represents the average size of the eigenvalues. However, we have used the smaller value of the second eigenvalue as 0.7 to account for sampling variability (Jackson, 1993). PROC VARCLUS identified clusters and computed 1-R² ratio ([1-R²_{owncluster}]/([1-R²_{nextclosest}])), which identifies a cluster of genotypes that are highly correlated among themselves and not highly correlated with genotypes in other clusters. The bullet graphs were generated for graphical summary of stability statistics, mean and BLUP of each genotype in different management practices across and within locations using SAS PROC GPLOT in conjugation with PROC GREPLAY of SAS v9.4.

3. Results

3.1. Variance analysis

The pooled analysis revealed statistically significant fixed effects (L, M, M × L) for grain yield (Table 2). The variance estimates of the yield for the year (Y) and the interaction between year and location (Y × L) were different (*P* < 0.01) from zero and accounted for 43% of the total variation. Except for G × Y and M × Y, estimates of the random effects were significant (ranged from 3 to 13% of the total variance estimate). Large estimate of environment (L × Y) variance dominated the expression of genotype effect (G) and interaction between genotype and management (G × M) (Table 2). Within location analysis, both fixed and random effects were significant in BR, MP and PB (Table 2). Year, G and G × M caused most of the variation in yield performance of wheat genotype in BR and MP (Table 2). In contrast, the temporal variance (Y) alone contributed the most in total variance for location PB. Across and

Table 2

Pooled variance analysis for wheat yield (t ha^{-1}) of 6 genotypes tested in 3 years and 3 locations over 10 management practices; and location variance of 10 genotypes tested for 3 years over 10 management practices.

Source	Pooled variance ^a		Location variance					
	F-ratio	% of total variance ^d	Bihar ^b		Madhya Pradesh ^c		Punjab ^b	
			F-ratio	% of total variance	F-ratio	% of total variance	F-ratio	% of total variance
Year (Y)		31.69*		15.25**		45.25***		73.19***
Location (L)	1.01*							
Y × L		10.98***						
Genotype (G)		2.39*		38.94***		2.61*		3.78**
G × Y		0.02NS		4.35***		6.00**		0.56
G × L		7.31***						
G × Y × L		2.07*						
Management (M)	6.43***		7.36***		2.64*		3.65**	
M × Y		1.00NS		17.29***		19.48***		7.84**
M × L	0.97*							
M × L × Y		12.22***						
G × M		3.71**		12.42***		7.62*		8.45*
G × M × Y		2.95*		11.75***		19.03***		6.28***
G × M × L		12.27*						
G × M × L × Y		12.84***						

*, **, and *** = significant at 0.05, 0.01, and 0.001 levels of probability, respectively; NS = non-significant. The value of significance presented in 'F-ratio' column represents *F* statistics *p*-values for *F*-ratio of fixed effects. Similarly, the value of significance presented in '% of total variance' column represents χ^2 statistics *p*-values of variance estimate of random effects.

^a Degrees of freedom: Y-2; L-2, Y × L-4; G-5; G × Y-10; G × L-10; G × Y × L-20; M-7; M × Y-14; M × L-14; M × L × Y-28; G × M-35; G × M × Y-70; G × M × L-70; G × M × L × Y-140.

^b Degrees of freedom: Y-2; G-9; G × Y-18; M-8; M × Y-16; G × M-72; G × M × Y-144.

^c Degrees of freedom: Y-2; G-9; G × Y-18; M-9; M × Y-18; G × M-81; G × M × Y-162.

^d % total variance is calculated by variance estimate of given effect divided by sum (total) of variance estimate of all the effects. List of effects used in model are presented in source column.

within locations, the estimate of G contributed to total variance ranged between 2.5–4.0%, except in location BR.

3.2. Polygon view of GGE biplot

The 'polygon' (which-won-where) view of the GGE biplot divides the biplot into sector via perpendicular lines (rays) passing from the polygon sides (Fig. 1). The polygon is drawn by joining extreme genotypes of the biplot. If environments fall into different sectors, then different genotypes won in different sectors, and a crossover G × E pattern exists. The winning genotype for an environment or set of environments in a sector is the vertex genotype. Conversely, if all environments fall into a single sector, a single genotype had the highest yield in all environments. The vertex genotype in a sector where no environment is present is considered to be a poor performer in all test environments. Genotypes within the polygon were less responsive to location than the vertex genotypes. Across locations, the polygon view of the GGE biplot explained 90, 84, 99, 97, 98, 97, 91 and 97% of the genotype and genotype × environment variation for the management practice D02, D03, D04, D05, D06, D07, D08 and D09, respectively (Fig. 1: Panel A to Panel H). Except for management practice D07, environments were grouped into two sectors with different winning (vertex) genotypes. This confirms the existence of G × E for all management practices, except for D07. However, the GGL biplots for individual year confirm that the location grouping varied across years for D07. Results of GGL are not presented here. Similarly, for location BR, MP and PB, a polygon view of GGE biplot revealed environments grouped into either 2 or 3 sectors across all the management practices. This suggest that different genotypes won in different sectors, and a crossover G × E pattern existed. Results of GGE are not presented here.

3.3. Genotype BLUPs

Across and within individual location(s), the actual mean yield tend to fall toward the late sowing (Fig. 2). However, the mean predicted yield (BLUP) tend to converge around management practice D04 to D06

across locations and for location BR and MP (Fig. 3). For location PB, the pattern of predicted yield was more zig-zag across management practices. Interestingly, for across and within location(s), both the actual and predicted yield agreed to the presence of large range between the maximum and minimum values of yield during the earliest planting. However, the highest actual and predicted yielding genotype is not same across and within location(s). BLUPs are the estimates of random effects. Across locations, estimates of genotype (random effect) for wheat yield ranged from 5.18 to 5.72 t ha^{-1} (Fig. 3, Supplemental Table 1 and Supplemental Fig. 3). The highest yield was estimated for genotype 'CSW 18' (G03) for management practice D02. Similarly, genotypes 'BAZ' (G01); 'CSW 16' (G02); and 'HD 2967' (G14) recorded high yield at D07; D08 and D09; and D02, D03 and D04, respectively (Fig. 2, Supplemental Table 1 and Supplemental Fig. 3).

Within individual location and across management practices, the mean predicted yield ranged from 4.61–6.39 t ha^{-1} , 4.82–5.53 t ha^{-1} , and 5.34–5.43 t ha^{-1} for location BR, MP and PB, respectively (Fig. 3, Supplemental Table 2, Supplemental Figs. 4–6). The high yielding genotypes were 'CSW 18' (G03) with D02, 'Munal' (G19) with D01 and 'CSW 18' (G03) with D05 for location BR, MP and PB, respectively.

3.4. Mean vs stability view of GGE biplot and bullet graphs

The 'average environment coordinate' (AEC) view based on genotype-focused singular value partitioning (SVP = 1) can be referred to as the 'mean vs. stability' view (Yan et al., 2007) of GGE biplot. That view facilitates genotype comparisons based on mean performance and stability across environments within a mega-environment. The 'mean vs. stability' view of GGE biplot explained 84–99% of genotypic and genotype × environment variation across locations under different management practices: D01–D10 (Fig. 4: Panel A to H). The arrow shown on the AEC abscissa points in the direction of higher yield performance of genotypes and ranks the genotypes with respect to yield performance. Thus, genotype 'HD 2967' (G14) had the highest yield in all the management practices, except for D03. Genotype 'Munal' (G19) had the highest yield in D03 (Fig. 4: Panel B). The stability of each genotype

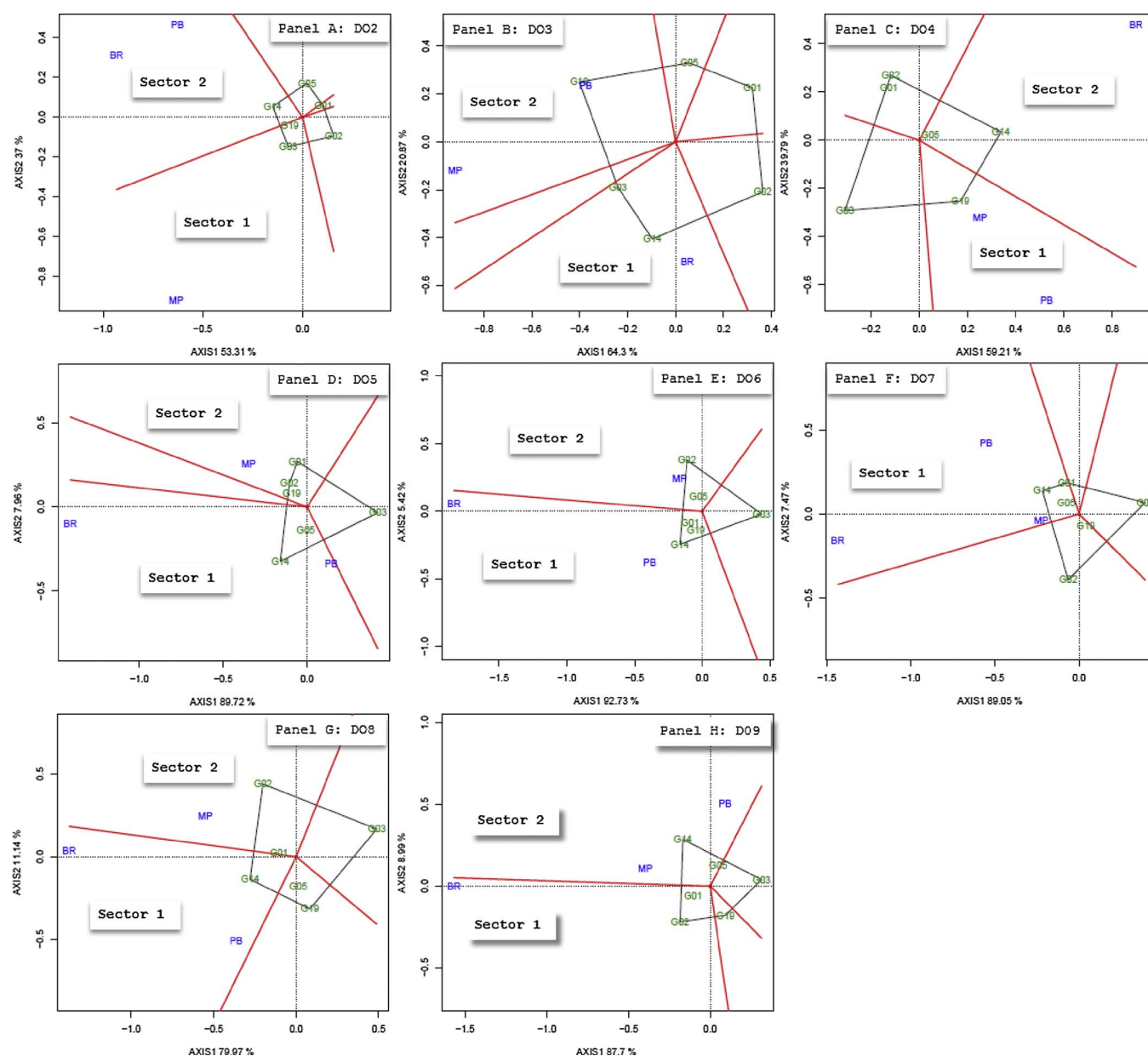


Fig. 1. The polygon (which-won-where) view of genotype main effects plus genotype \times environment interaction effect (GGE) biplot of yield of 6 wheat genotypes tested in 3 years, 3 locations over 8 management practices (Panel A to Panel H). The biplots were based on Scaling = 0, Centering = 0, and SVP = 2. Key to the labels of genotype, management practices and location is presented in abbreviation section.

was explored by its projection onto the AEC vertical axis. The most stable genotype was located almost on the AEC abscissa (horizontal axis) and had a near-zero projection onto the AEC (vertical axis). Thus, in management practice D08 ‘BAZ’ (G01) and ‘CSW 16’ (G02) were the most and least stable, respectively (Fig. 4: Panel G). We have summarized the across and within location stability results using color code in bullet graphs (Figs. 5–8). Back ground fill color of green, yellow and violet within each horizontal bar represent high, medium and low stability. The stability color-genotype-management practice-yield performance matrix in bullet graph provides user to quickly identify the stability and yield performance simultaneously across the management practices. Thus, under management practice D02 genotype ‘BAZ’ (G01) was high stable across locations, in location BR and in location MP, and low stable in location PB (Panel A of Figs. 5–8). Likewise, genotype ‘CSW-16’ (G02) was stable in management practice D05; D03, D04 and D05; D03, D06, D09 and D10; and D06 across locations, location BR, location MP and location PB, respectively. Overall, the pattern of

genotype stability varied across management practice in within and across location analysis.

3.5. Divisive clusters and $1-R^2$ ratio

Across locations under all management practices (except D02 and D08), similarly performing genotypes were grouped into two clusters (Table 3). In D02 and D08 genotypes were grouped into 4 and 1 clusters, respectively. The most representative and distinct genotype within the cluster has high correlation with its own cluster and low correlation with other clusters (SAS, 2017). Thus, an ideal representative genotype has a low $1-R^2$ ratio ($[1-R^2_{\text{owncluster}}]/[1-R^2_{\text{nextclosest}}]$) value. Across all the tested location, in cluster 1 of D02, ‘HD 2967’ (G14) had the lowest $1-R^2$ ratio (0.24) and, thus, was the representative genotype (Table 3). The cluster 2, cluster 3 and cluster 4 of D02 consist of single distinct genotype with zero value of $1-R^2$ ratio (Table 3). It means that the genotype in each cluster is distinctive in yield performance when compared with

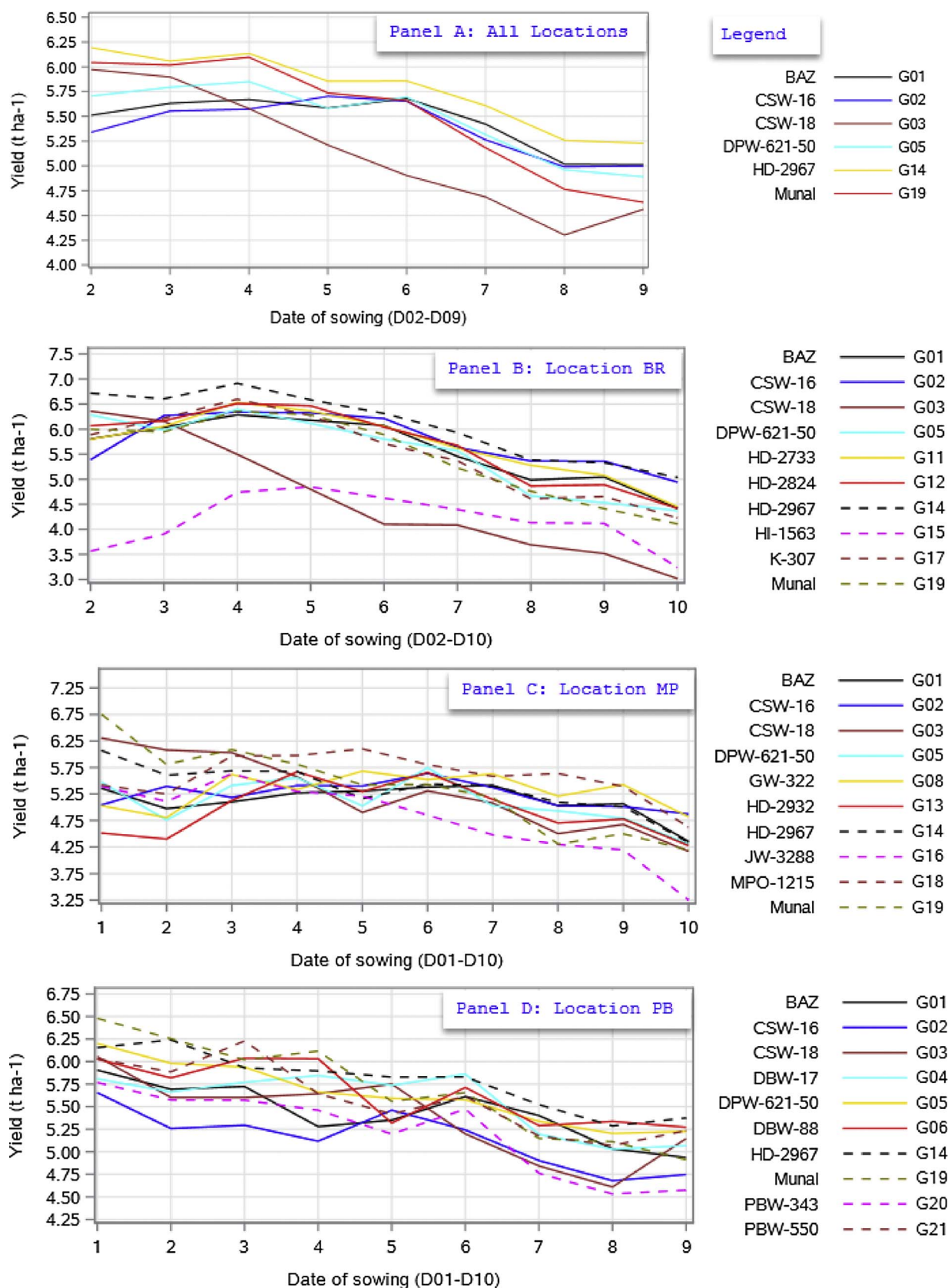


Fig. 2. Yield performance of wheat genotypes tested for 3 years over 10 management practices (variable DOS) across locations (Panel A) and at location BR (Panel B), MP (Panel C) and PB (Panel D).

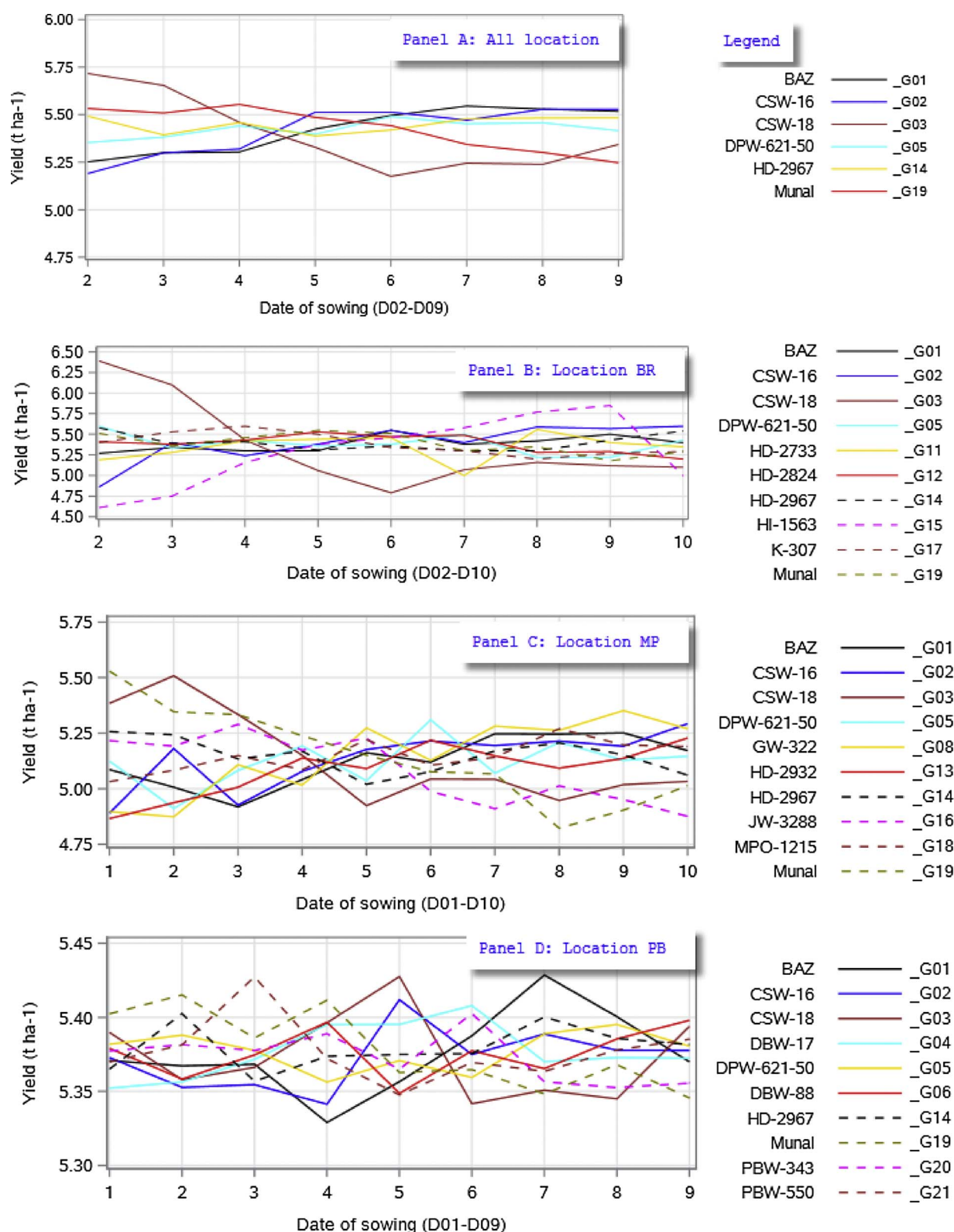


Fig. 3. BLUP of yield of wheat genotypes tested for 3 years over 10 management practices across locations (Panel A) and at location BR (Panel B), MP (Panel C) and PB (Panel D).

rest of the clusters. The zero value of $1-R^2$ ratio is the result of the presence of a single entity in the cluster and, thus, correlation within its own cluster is 1 ($[(1-1)/[(1-R^2_{\text{nextclosest}})] = 0/[(1-R^2_{\text{nextclosest}})] = 0$). Likewise, single genotype 'CSW 18' (G03) forms a cluster 2 in D04, D05, and D06. Similarly, in D03 genotype 'BAZ' (G01), 'CSW 16' (G02) and 'CSW 18' (G03) represented cluster 1 and had same

value of $1-R^2$ ratio (0.34) (Table 3). Thus, all three genotypes were equally representative. Genotype 'DPW 621-50' (G05) were representative for cluster 2 in D03 (Table 3). Likewise, in D08 all 6 genotypes performed equally and, thus, grouped into single cluster (Table 3). For location BR, genotypes were grouped into 1–5 clusters across management practices (Table 4). The differential performance of

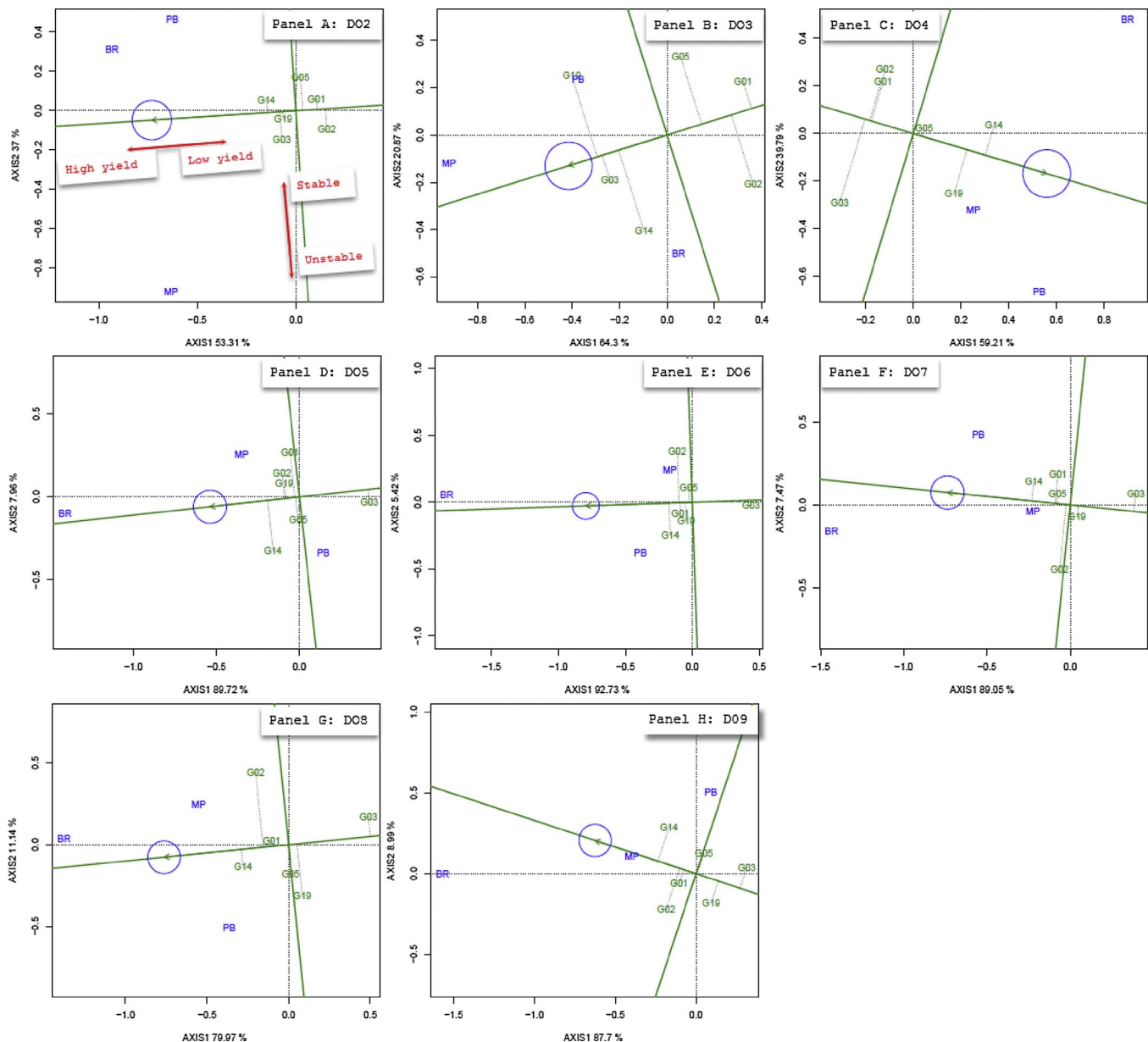


Fig. 4. The mean vs. stability view of genotype main effects plus genotype \times environment interaction effect (GGE) biplot of yield of 6 wheat genotypes tested in 3 years, 3 locations over 8 management practices (Panel A and Panel H). The biplots were based on Scaling = 0, Centering = 0, and SVP = 2. Key to the labels of genotype, management practices and location is presented in abbreviation section.

genotypes minimized in later sowing dates. Thus, in D10 all genotypes were grouped into 1 cluster (Table 4). Similarly, for location MP, genotypes were grouped into 2–5 clusters. Majority of the clusters were constituted with ≥ 2 genotypes, except 1, 1, 1 and 3 clusters in D02, D03, D04 and D05, respectively (Table 5). In location PB, genotypes were grouped into 1, 2 and 3 clusters for D06 to D09; D01, D02, D03, D04 and D06; and D05, respectively (Table 6). Grouping of genotypes to form clusters and representative genotype within each cluster are not consistent across management practices (D01–D10) in each location (Table 4–6).

4. Discussion

Wheat genotypes used in our study were genetically established to be grown in environments of Indo-Gangetic plains under conventional sowing dates, where crop duration, temperature and precipitation variance are lately inconsistent. Routine multi-locations and –year

trials are commonly practiced among agronomist and breeders to identify reliable performing genotypes. However, comparing our findings – on the effects of shifted sowing dates on varietal adaptation – with similar research is slightly challenging by degeneration or absence of data. A number of studies conducted on G \times E in many crops and mostly agree with the existence of temporal and spatial environment variability and their influence on inferences and recommendation for varietal adoption and commercialization. The total variance of multi-environment trial data can be partitioned among experimental factors and their interaction effects. In our study across locations, the F ratio of the fixed effects (L, M, M \times L) was statistically significant. The mean yield of genotypes for the crop management practices (M) varied across D02–D09 and locations (Figs. 2 and 5), and these results are in agreement with our previous findings (Dhillon and Ortiz-Monasterio, 1993; Ahmed and Fayyas-ul-Hassan, 2015). The significant M \times L suggests a variable response of genotype yield to the shifted dates of sowing across the test locations. Except for G \times Y and M \times Y, estimates of the random

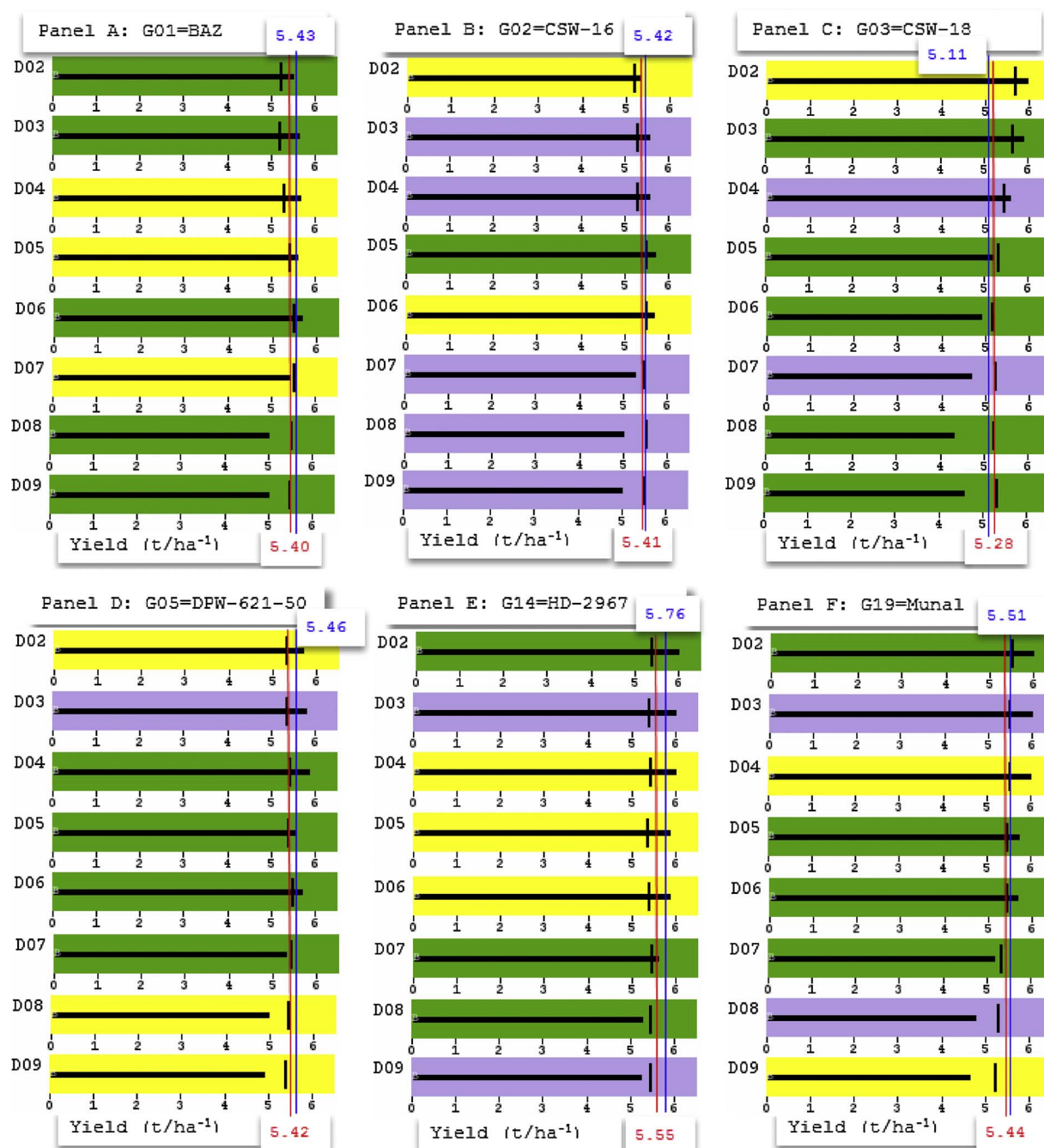


Fig. 5. Bullet graph summary of stability statistics, mean yield across and within management practice(s), and BLUP yield across and within management practice(s) of 6 wheat genotypes (Panel A to Panel F) tested in 3 years, 3 locations over 8 management practices. The horizontal bars represent management practices (D02–D09). Back ground fill color of green, yellow and violet within each horizontal bar represent high, medium and low stability. The horizontal and vertical black line within each horizontal bar measure genotype mean and BLUP yield, respectively, on quantitative scale (x-axis, $t\ ha^{-1}$). The blue and red vertical lines across horizontal bar represent genotype mean and BLUP yield across management practices. Key to the labels of genotype and management practices is presented in abbreviation section. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

effects were significant (Table 2). Similar results were reported in the study by Alam et al. (2013), Mumtaz et al. (2015), Nwofia et al. (2016). The estimates of random effects varied from 0.02–32% of the total variance. The large estimates of Y and Y \times L suggest that the agro-ecological conditions of the test locations were extremely different and accounted for most of the yield variation. The small contribution of G in the total variance estimate is due to the fact that genotypes evaluated in this study were advanced breeding lines, elite cultivars or high yielding genotypes. The significant variance components for G \times M, G \times M \times L and G \times M \times L \times Y led to a different ranking of genotypes across environments under shifted sowing dates (D02–D08), justifying the

development of a stable genotype that performs well over environments in different management practices. The ideal genotype should have a high trait performance and high stability. Significant G \times Y \times L suggests the existence of divergence performance of genotype across year and location. Furthermore, the significant G \times M at individual location suggest the importance of identifying location and management specific stable genotypes.

Normally, the average temperature tends to decrease from D01 to D10 at all the three locations (Supplemental Fig. 7). However, recent studies suggest that global average temperature is expected to rise due to climate change, and is already contributing to the global burden of

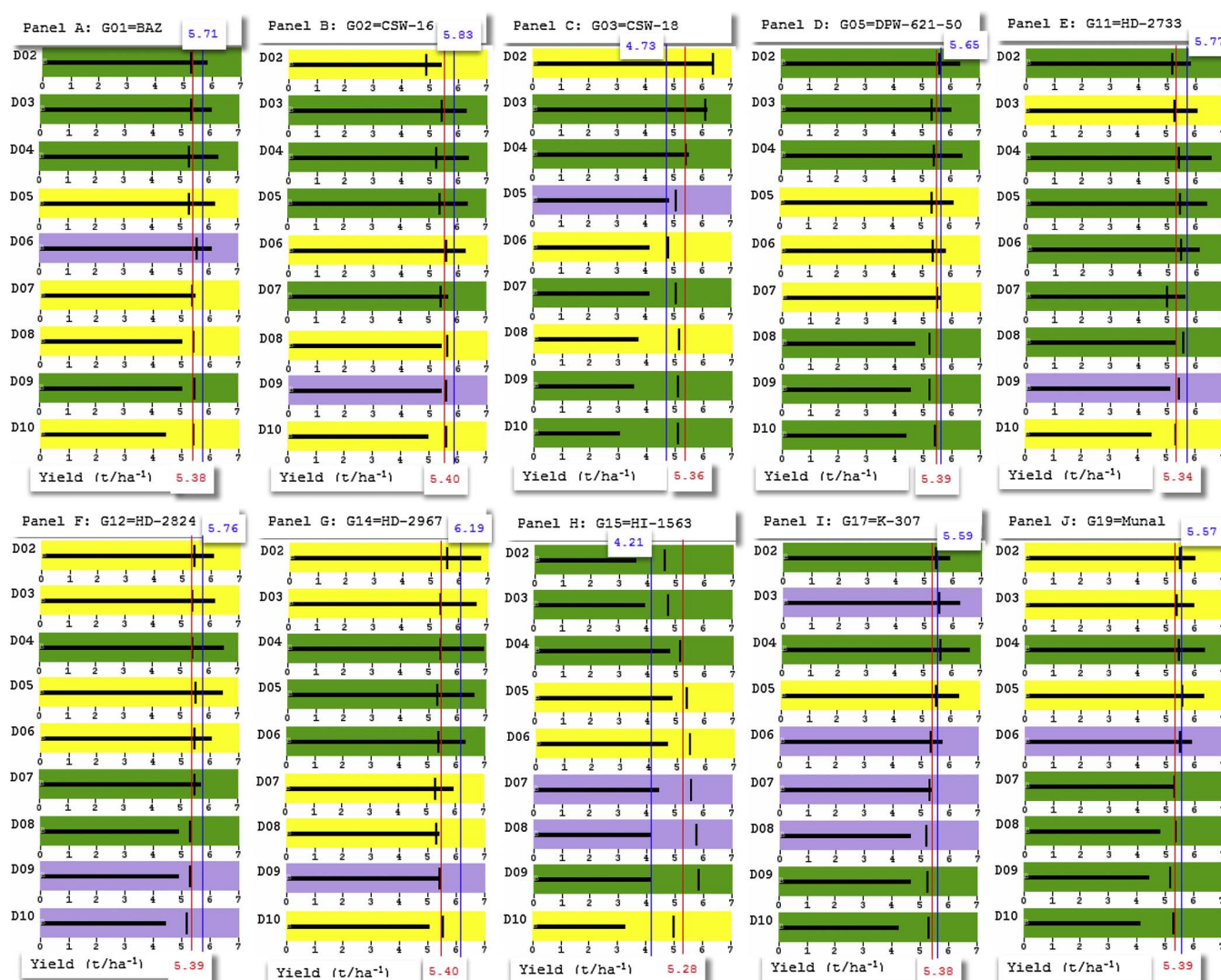


Fig. 6. Bullet graph summary of stability statistics, mean yield across and within management practice(s), and BLUP yield across and within management practice(s) of 10 (6 same + 4 different) wheat genotypes (Panel A to Panel J) tested in 3 years over 9 management practices in location BR. The horizontal bars represent management practices (D02–D10). Background fill color of green, yellow and violet within each horizontal bar represent high, medium and low stability. The horizontal and vertical black line within each horizontal bar measure genotype mean and BLUP yield, respectively, on quantitative scale (x-axis, t/ha^{-1}). The blue and red vertical lines across horizontal bar represent genotype mean and BLUP yield across management practices. Key to the labels of genotype and management practices is presented in abbreviation section. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

reduced crop productivity and stability (Lobell et al., 2011). Experimental work by Lobell et al. (2011) pooled analyzed the 20,000 historical maize trial data along with meteorological data, revealed that each degree-day spent above $30^{\circ}C$, the final yield was reduced by 1% under optimal rain-fed conditions and 1.7% under drought conditions. Similarly, wheat yields are reduced 3–4% per $1^{\circ}C$ rise above the optimum temperature (15 – $20^{\circ}C$) during grain filling (Wardlaw et al., 1989). Based on these evidences, we assumed that the temperature in Indo-Gangetic plains during crop duration, including across management practices (D01 to D10), were slightly increased but the pattern remained same as normal. Therefore, understanding the specific impacts of shifted sowing dates and elevated temperature on wheat yield stability in Indo-Gangetic plains is important. Based on early (October: D01–D03), normal (November: D04–D07) and late (December: D08–D10) sowing dates we identified differentially stable genotypes for each of these 3 categories. Across locations, during early planting the number of divisive clusters decreased from 4 to 2 for D02 to D03 (early planting), respectively (Table 3). In other words, similar performing genotypes changed as date of sowing shifted from D02 to D03. More number of clusters in D02 than D03 suggest the differential

performance of genotypes were prominent at early sowing. Singh et al. (2016a, 2016b) reported that during early planting the lower grain yield was associated with lower grain number due to shorter vegetative growth period, lower leaf area index and biomass production. These findings are further corroborated with the fluctuating pattern of actual yield among genotypes from D02 to D03 (Fig. 2: Panel A). Interestingly, the pattern of actual yield and predicted yield of all the tested genotypes from D02 to D03 remained same (Figs. 2 and 3: Panel A). Similarly, the grouping of genotypes in forming clusters varied from D02 to D03 (Table 3). The different grouping patterns suggest the existence interaction of shifted sowing dates with different genetic composition, plant architecture, and stress tolerant and disease resistance levels of genotypes (Table 1). A decision to select the most representative and distinct genotype within the cluster must be based on the low value of $1-R^2$ ratio. The duplicate $1-R^2$ ratio values of genotype within the cluster provide the same information (redundancy exist) and can be used interchangeably to reduce testing costs and improve efficiency of breeding programs. Thus, genotype ‘HD 2967’ (G14) was the most representative and distinct genotype in cluster 1 of D02 whereas in cluster 1 of D03 genotypes ‘BAZ’ (G01), ‘CSW 16’ (G02) and ‘CSW 18’ (G03)

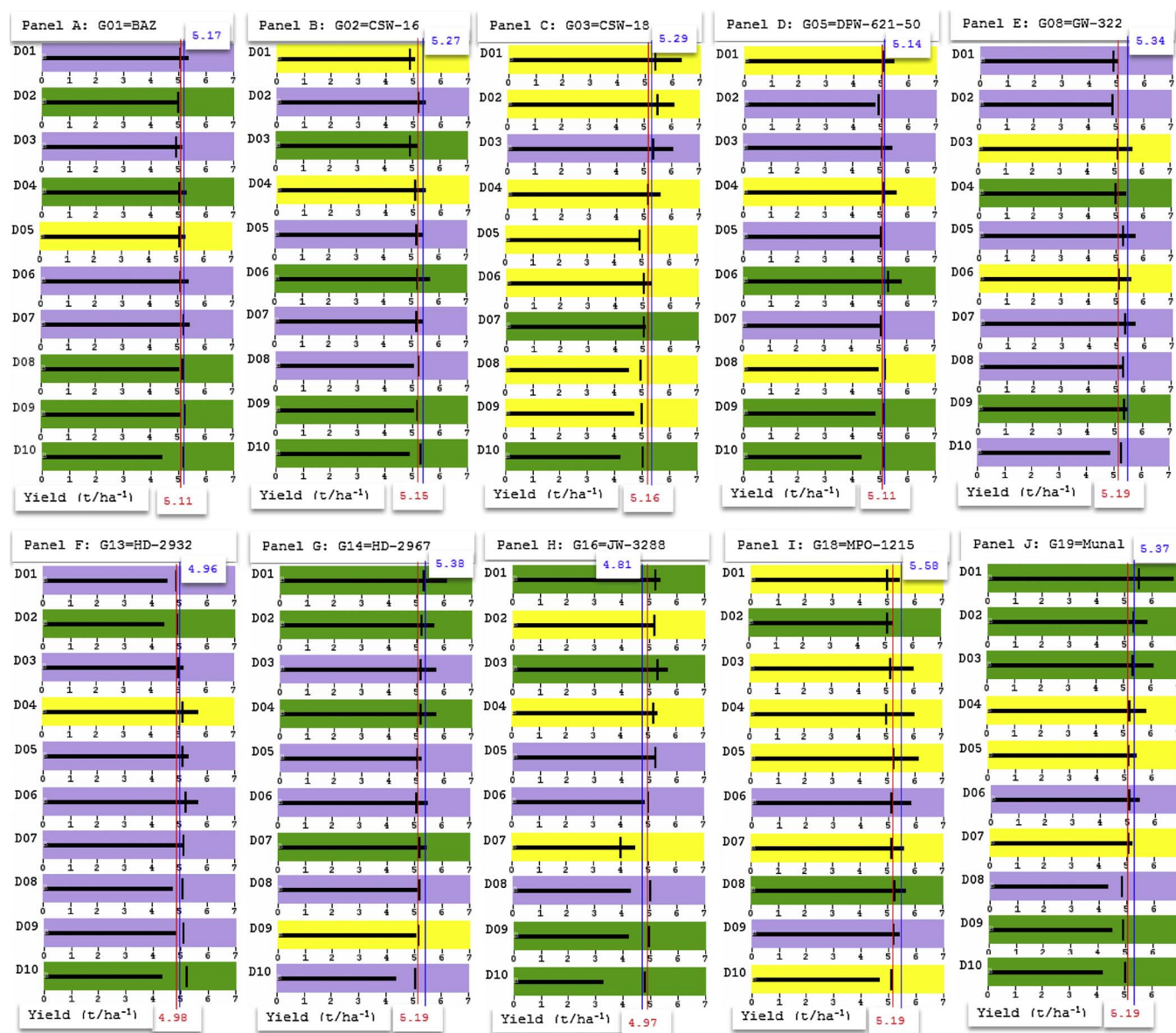


Fig. 7. Bullet graph summary of stability statistics, mean yield across and within management practice(s), and BLUP yield across and within management practice(s) of 10 (6 same + 4 different) wheat genotypes (Panel A to Panel J) tested in 3 years over 10 management practices at location MP. The horizontal bars represent management practices (D01-D10). Back ground fill color of green, yellow and violet within each horizontal bar represent high, medium and low stability. The horizontal and vertical black line within each horizontal bar measure genotype mean and BLUP yield, respectively, on quantitative scale (x-axis, t ha⁻¹). The blue and red vertical lines across horizontal bar represent genotype mean and BLUP yield across management practices. Key to the labels of genotype and management practices is presented in abbreviation section. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

had same $1-R^2$ ratio values (equally representative and distinctive) and, hence, they can be used interchangeably. Additionally, wheat breeders can use the most representative and distinct genotype as a diverse parent for future breeding purposes to exploit the genetic variability.

Two distinct process can characterize a plant's life cycle: development and growth. Development is a process directly related to the phenology of the genotype, which is primarily driven by temperature. Development determines if a genotype is adapted to an environment. Adaptation, the timing of key developmental stages such that the genotype can maximize benefit from environmental conditions, is key for maximizing growth. Growth is the process of biomass accumulation, which is driven primarily by light interception of the plant (solar radiation) and limited by the plant's available nitrogen and water status. As growth and development are distinctly different processes, it is reasonable to expect that $G \times E$ effects arising from them could have substantially different consequences (Lee et al., 2016). Based on

multiple parameters (stability, divisive clusters, predictive yield), we categorized genotypes into three categories. Category 1 genotypes had high representativeness, high to medium predictive yield and high to medium stability. These genotypes are widely adopted across varied environmental conditions including sowing dates. Category 2 genotypes had high to medium predictive yield but low stability. These genotypes are sensitive to environmental change and had greater specificity of adaptability to high yielding environments. Category 3 genotypes had medium to low predictive yield and low stability. These genotypes are suitable for traits (other than yield) such as disease or lodging resistance, where low values are desired in high yielding environments. Thus, for early sowing dates (D02-D03) 'CSW 18' (G03); 'HD 2967' (G14) and 'Munal' (G19); and 'BAZ' (G01) were category 1, category 2 and category 3 genotypes, respectively (Fig. 5). In early planting, stability and productivity may be limited with differential sensitivity of genotype to low temperature and low solar radiation during pre-

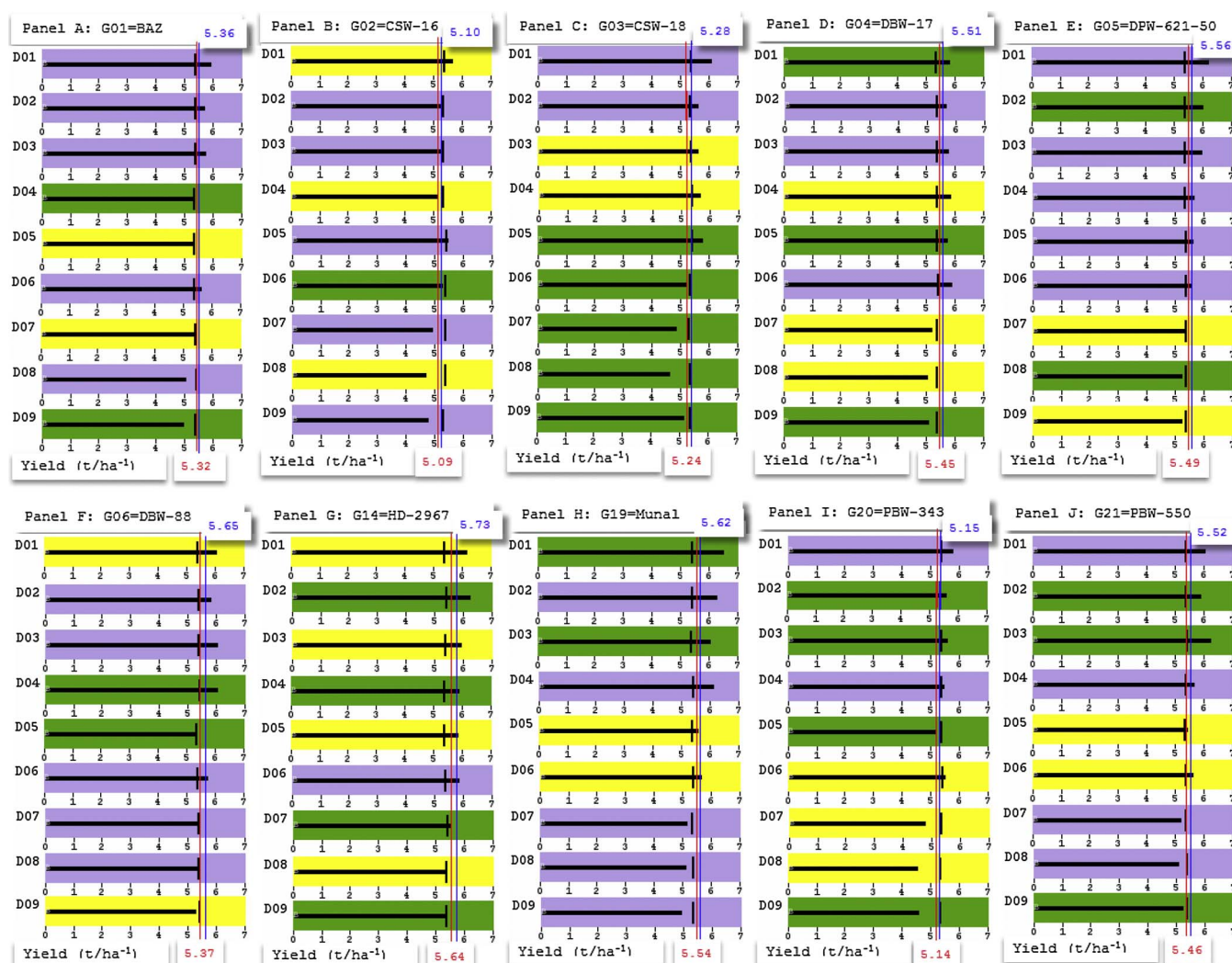


Fig. 8. Bullet graph summary of stability statistics, mean yield across and within management practice(s), and BLUP yield across and within management practice(s) of 10 (6 same + 4 different) wheat genotypes (Panel A to Panel J) tested in 3 years over 9 management practices in location PB. The horizontal bars represent management practices (D02–D10). Background fill color of green, yellow and violet within each horizontal bar represent high, medium and low stability. The horizontal and vertical black line within each horizontal bar measure genotype mean and BLUP yield, respectively, on quantitative scale (x-axis, $t\ ha^{-1}$). The blue and red vertical lines across horizontal bar represent genotype mean and BLUP yield across management practices. Key to the labels of genotype and management practices is presented in abbreviation section. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

anthesis period and the interaction with the disease development. Alam et al. (2013) found that early planting increased the severity of foliar diseases and, thus, reduced the yield. Pedigree of 'BAZ' (G01) suggests that it has capability to withstand stem rust, Ug99 and heat stress. Therefore, researchers can introgress genes from 'BAZ' into elite inbreds to make better high hybrids with high stability.

Similarly, during normal sowing dates (D04–D07) number of divisive clustered formed were same (Table 3). The pattern of genotype grouped in each cluster remained consistent, except in D07. This suggest that from D04 to D06 environment had similar influence on the performance of all the 6 tested genotypes. However, distinct values of $1-R^2$ ratio in each cluster indicated the existence of some extent of dissimilarity among genotypes within the cluster (Table 3). This finding can be further corroborated with the unique genetic makeup of or distinct parents being used in each genotype (Table 1). The predicted yield of low and high performing genotypes flipped while the average performing genotype remained same from D04 to D07 (Fig. 3: Panel A). This suggest that the early planted high performing genotypes were more sensitive to terminal heat stress as the date of sowing is delayed. Usually plants employ various physiological adaptive mechanisms such as high-transpiration rate, earliness, stay-green and reduced

photosynthetic rates (Cornish et al., 1991; Reynolds et al., 1998) to escape or adapt to terminal heat stress. These mechanism might have played key roles for low performing and early planted genotypes to perform well during late planting. Heat stress induce decrease in the duration of developmental phases leading to fewer organs, smaller organs, reduced light perception over the shortened life cycle and perturbation of the processes related to carbon assimilation (transpiration, photosynthesis and respiration) are significant contributing to losses of yield (Rane and Chauhan, 2002; Hussain and Mudasser, 2007).

Genotypes 'DPW 621-50' (G05) and 'HD 2967' (G14) qualified for category 1 and category 2 genotypes, respectively, for normal sowing dates. None of the tested genotypes qualified for category 3 genotypes. In D04–D07, stability and productivity might be limited with reduced grain m^{-2} or reduced thousand kernel weight caused by high temperature during pre- and post-anthesis. DuPont et al. (2006) found that high temperatures during grain growth shortened and compressed stages of grain filling, reduced duration of dry matter accumulation and reduced kernel weight by 50%.

Likewise, during later sowing dates (D08–D09), the number of divisive cluster(s) increased from 1 to 2. Relatively, overall actual yield decreased as sowing dates are pushed back. These finding are in

Table 3Divisive cluster and 1-R² ratio of yield of 6 wheat genotypes tested in 3 years, 3 locations over 8 management practices.

Date of sowing	Total Cluster	All location			
		Genotype 1-R ² ratio			
		Cluster1	Cluster2	Cluster 3	Cluster 4
D02	4	G01, G05, G14 0.29, 0.32, 0.24	G02 0.00	G19 0.00	G03 0.00
D03	2	G01, G02, G03 0.34, 0.34, 0.34	G05, G14, G19 0.17, 0.37, 0.50	–	–
D04	2	G01, G02, G05, G14, G19 0.14, 0.25, 0.21, 0.13, 0.38	G03 0.00	–	–
D05	2	G01, G02, G05, G14, G19 0.33, 0.23, 0.13, 0.10, 0.31	G03 0.00	–	–
D06	2	G01, G02, G05, G14, G19 0.10, 0.39, 0.28, 0.10, 0.17	G03 0.00	–	–
D07	2	G02, G05, G14 0.51, 0.17, 0.21	G01, G03, G19 0.33, 0.24, 0.36	–	–
D08	1	G01, G02, G03, G05, G14, G19 0.00, 0.00, 0.00, 0.00, 0.00, 0.00	–	–	–
D09	2	G01, G02, G14 0.35, 0.21, 0.42	G03, G05, G19 0.20, 0.09, 0.49	–	–

Table 4Divisive cluster and 1-R² ratio of yield of location BR for yield of 10 (6 same + 4 different) wheat genotypes tested for 3 years over 9 management practices.

Date of sowing	Total Cluster	Location: BR				
		Genotype 1-R ² ratio				
		Cluster1	Cluster2	Cluster 3	Cluster 4	Cluster 5
D02	5	G01, G02, G05, G17 0.34, 0.38, 0.09, 0.36	G12, G19 0.03, 0.02	G11 0.00	G03, G15 0.13, 0.15	G14 0.00
D03	4	G02, G11, G12, G19 0.09, 0.09, 0.10, 0.05	G01, G14, G15, G17 0.01, 0.31, 0.05, 0.40	G03 0.00	G05 0.00	–
D04	5	G05, G14, G19 0.14, 0.25, 0.21	G01, G11, G17 0.42, 0.25, 0.34	G03 0.00	G02, G12 0.39, 0.34	G15 0.00
D05	4	G02, G11, G12, G17 0.17, 0.18, 0.02, 0.11	G03, G05, G01 0.17, 0.29, 0.12	G14 0.00	G15, G19 0.25, 0.38	–
D06	3	G01, G05, G15, G19 0.20, 0.09, 0.20, 0.39	G02, G11, G12, G17 0.04, 0.58, 0.07, 0.27	G03, G14 0.05, 0.04	–	–
D07	2	G02, G05, G12, G14, G17 0.63, 0.13, 0.17, 0.50, 0.15	G01, G03, G11, G15, G19 0.17, 0.29, 0.66, 0.33, 0.33	–	–	–
D08	2	G01, G02, G12, G14, G17 0.10, 0.07, 0.09, 0.35, 0.61	G03, G05, G11, G15, G19 0.64, 0.07, 0.11, 0.53, 0.31	–	–	–
D09	2	G02, G03, G05, G11, G15, G19 0.06, 0.01, 0.14, 0.07, 0.12, 0.01	G01, G12, G14, G17 0.12, 0.06, 0.56, 0.02	–	–	–
D10	1	G01, G02, G03, G05, G11, G12, G14, G15, G17, G19 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00	–	–	–	–

agreement with [Ortiz-monasterio et al. \(1994\)](#), who reported decreased grain yield by 0.8% per day delay after Nov 15 in Punjab. However, the low performing genotypes in early sowing dates (D02-D03) tend to have increased predictive yield in late sowing dates. Exceptionally, genotype ‘BAZ’ (G01), ‘CSW 16’ (G02) had predictive yield higher than average BLUP across management practices (Supplemental Fig. 3). Genotype ‘BAZ’ (G01), ‘CSW 16’ (G02) and ‘Munal’ (G19) qualified for category 1, category 2 and category 3 genotypes, respectively, for late sowing dates. During delayed sowing wheat is drastically affected not only in germination but also growth behavior, leaf area development, number of tillers, number of grains per spike, and thousand kernel weight and eventually the grain yield. Therefore, the high-yield stability and productivity is early establishment and source-limited. Conversely, [Ahmed and Fayyas-ul-Hassan \(2015\)](#) found that under delayed sowing lower yield is often accompanied with improved quality traits like proline, grain ash and grain protein. The increased grain protein under delayed sowing is directly related to high temperature and water stress by modifying source-sink balance ([Motzo et al., 2007](#)). Thus,

category 3 genotypes, like ‘Munal’ (G19), is recommended for high quality low yield stable wheat genotypes under delayed sowing.

In location BR, the pattern of number of cluster, actual yield and predicted yield convergence across management practice is akin to across locations analysis. Number of clusters decreased from early to late sowing dates ([Table 4](#)). Similarly, the predicted yield converged as sowing dates shifted from early to normal. During later sowing dates, predicted yield pattern flipped and tends to disperse ([Fig. 3](#): Panel B). For early sowing dates all the tested genotypes had medium to high stability ([Fig. 6](#)). Genotype ‘CSW 18’ (G03) and ‘DPW 621-50’ (G05) were the most distinctive, and had high predictive yield and high stability. Therefore, these genotype qualified for category 1. Category 2 genotypes were ‘HD 2967’ (G14) and ‘Munal’ (G19). For normal sowing dates (G04-G07), ‘HD 2733’ (G11), ‘HI 1563’ (G15) and ‘K 307’ (G17), and ‘BAZ’ (G01) were category 1, category 2 and category 3 genotypes, respectively. Genotype ‘HI 1563’ (G15) had predicted yield higher than average BLUP across D02-D10 (Supplement Fig. 4). For late sowing dates (D08-D10), ‘CSW 18’ (G03) and ‘DPW 621-50’ (G05), ‘HD 2733’

Table 5Divisive cluster and 1-R² ratio of yield of locations MP for yield of 10 (6 same + 4 different) wheat genotypes tested for 3 years over 10 management practices.

Date of sowing	Total Cluster	Location: MP				
		Genotype 1-R ² ratio				
		Cluster1	Cluster2	Cluster 3	Cluster 4	Cluster 5
D01	4	G01, G05, G08, G18 0.09, 0.05, 0.04, 0.07	G13, G16 0.06, 0.11	G02, G14 0.15, 0.39	G03, G19 0.04, 0.05	–
D02	4	G03, G05, G08, G13 0.17, 0.34, 0.31, 0.02	G14, G16, G18 0.03, 0.07, 0.18	G01, G02 0.35, 0.17	G19 0.00	–
D03	3	G01, G02, G03, G14, G16 0.29, 0.16, 0.23, 0.32, 0.12	G05, G08, G13, G18 0.19, 0.41, 0.32, 0.24	G19 0.00	–	–
D04	2	G01, G03, G05, G08, G13, G14, G16, G18, G19 0.13, 0.15, 0.01, 0.03, 0.16, 0.25, 0.01, 0.03, 0.03	G02 0.00	–	–	–
D05	5	G01, G05, G08 0.01, 0.01, 0.03	G02, G03, G13, G18 0.40, 0.23, 0.01, 0.12	G19 0.00	G16 0.00	G01 0.00
D06	2	G01, G08, G14, G16, G18, G19 0.26, 0.21, 0.06, 0.40, 0.10, 0.09	G02, G03, G05, G13 0.21, 0.12, 0.05, 0.26	–	–	–
D07	3	G01, G02, G08, G16 0.09, 0.26, 0.62, 0.02	G03, G13, G14 0.12, 0.11, 0.20	G05, G18, G19 0.48, 0.17, 0.34	–	–
D08	3	G08, G13, G14, G16, G18 0.23, 0.33, 0.20, 0.07, 0.21	G02, G05 0.06, 0.04	G01, G03, G19 0.31, 0.28, 0.05	–	–
D09	2	G08, G13, G16, G18, G19 0.27, 0.07, 0.01, 0.05, 0.01	G01, G02, G03, G05, G14 0.36, 0.03, 0.04, 0.04, 0.14	–	–	–
D10	3	G03, G08, G14, G16, G19 0.26, 0.05, 0.61, 0.03, 0.06	G02, G05, G18 0.09, 0.20, 0.36	G01, G03 0.07, 0.07	–	–

Table 6Divisive cluster and 1-R² ratio of yield of location PB for yield of 10 (6 same + 4 different) wheat genotypes tested for 3 years over 9 management practices.

Date of sowing	Total Cluster	Location: PB		
		Genotype 1-R ² ratio		
		Cluster1	Cluster2	Cluster 3
D01	2	G01, G02, G03, G05, G14, G19, G21 0.01, 0.04, 0.21, 0.01, 0.03, 0.18, 0.03	G04, G06, G20 0.07, 0.19, 0.03	–
D02	2	G01, G03, G05, G06, G19, G20, G21 0.42, 0.29, 0.09, 0.62, 0.16, 0.44, 0.29	G02, G04, G14 0.31, 0.30, 0.32	–
D03	2	G01, G02, G03, G05, G06, G14, G19, G20 0.08, 0.48, 0.18, 0.10, 0.28, 0.02, 0.05, 0.10	G04, G21 0.06, 0.09	–
D04	2	G01, G02, G03, G04, G05, G06, G14, G19 0.18, 0.05, 0.09, 0.19, 0.09, 0.06, 0.09, 0.03	G20, G21 0.01, 0.01	–
D05	3	G02, G03, G05, G06, G20 0.20, 0.19, 0.07, 0.20, 0.38	G01, G04, G14, G21 0.05, 0.42, 0.08, 0.11	G19 0.00
D06	2	G01, G02, G03, G05, G06, G14, G19, G20, G21 0.26, 0.25, 0.16, 0.04, 0.10, 0.12, 0.04, 0.38, 0.10	G04 0.00	–
D07	1	G01, G02, G03, G04, G05, G06, G14, G19, G20, G21 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00	–	–
D08	1	G01, G02, G03, G04, G05, G06, G14, G19, G20, G21 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00	–	–
D09	1	G01, G02, G03, G04, G05, G06, G14, G19, G20, G21 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00	–	–

(G11), and ‘CSW 16’ (G02) and ‘HD 2824’ (G12) were category 1, category 2 and category 3 genotypes, respectively.

In location MP, both the actual and predicted yield of all tested genotypes fluctuated across D01 to D10, and changed the rank around D04 and D05 (Fig. 2: Panel C and Fig. 3: Panel C). Unlike the location BR, the number of clusters and pattern of genotype grouping in clusters is not consistent across management practices (D01–D10). These findings suggest that impenetrable interaction between wheat yield and shifted sowing dates resulted in performance scale and rank shift. Furthermore, high frequency of violet color bars in stability bullet graph confirms the existence of frequent instability across D01 to D10 among all tested genotypes (Fig. 7). Violet color represent low stability (Fig. 7). For early sowing dates, ‘JW-3288’ (G16) and ‘Munal’ (G19), ‘CSW 18’ (G03), and ‘CSW 16’ (G02) and ‘GW 322’ (G08) were category 1, category 2 and

category 3 genotypes, respectively. During normal sowing dates (D04–D07), majority of the genotypes had medium to low stability. Thus, none of the genotypes were qualified for category 1. Genotype ‘JW-3288’ (G16) and ‘Munal’ (G19) were category 2 and category 3 genotypes, respectively. For late sowing dates, ‘BAZ’ (G01), ‘CSW 16’ (G02) and ‘DPW 621-50’ (G05); and ‘HD 2932’ (G13) and ‘Munal’ (G14) were category 1 and category 2 genotypes, respectively.

Alike location MP, the predicted yield in location PB fluctuated across D01 to D09 (Fig. 3: Panel D). Similarly, the performance of all the tested genotypes was mostly unstable across management practices (D01–D09), which is confirmed with high frequency of violet color bars in stability chart (Fig. 8). Number of divisive clusters recorded were consistent during early and normal sowing dates. In contrast, variability among genotype performance was same during late sowing dates

(D08-D10). Therefore, all the genotypes were grouped into single cluster (Table 6). It suggests that the grain yield variation from these interactions is the least important. For early sowing dates, 'PBW 343' (G20) and 'PBW 550' (G21), 'DBW 88' (G06) and 'CSW16' (G02), and 'BAZ' (G01) were category 1, category 2 and category 3 genotypes, respectively. Similarly, for normal sowing dates, 'CSW 18' (G03), 'DPW 621-50' (G05) and 'PBW 550' (G21) qualified for category 1, category 2 and category 3 genotypes, respectively. In comparison to BR, similar pattern of predicted yield and stability in MP and PB could be due to consistently found relatively lower values of meteorological parameters (like temperature, solar radiation, relative humidity) in these two locations (Supplemental Figs. 1 and 2). Nix (1976) showed that temperature and radiation influence plant processes differently, but there combined effect can be usefully described as a photothermal quotient (PTQ). Midmore et al. (1984) and Fischer (1985) observed that grains m^{-2} in wheat was associated with PTQ over 30 days preceding anthesis. The theory behind the PTQ is based on the assumption that radiation and temperature are the driving forces in assimilate production and development rate, respectively, during this critical phase (Dhillon and Ortiz-Monasterio, 1993).

This study suggest that quantifying the effects of shifted sowing dates on yield stability is a complex exercise, due to multiple casual pathways leading to scale and rank shift of trait performance. The intricate interactions of shifted sowing dates with the, but not limited to, temperature variation, solar radiation fluctuation, change in precipitation pattern and soil moisture, seasonal climate pattern (drought and flood) and pest incidence exacerbate the reduced performance of crop bio-system. To fully understand the aggregate impact of climate change, including elevated temperature, on yield stability in Indo-Gangetic plains it is important to consider intense research, which includes (but not limited to) historical and current meteorological data, dense multi-environment trials, information on critical vegetative and reproductive stages (phenological stages) and disease data using high throughput phenotyping such as unmanned aerial vehicle (Mohan et al., 2017). By categorizing the performance and stability based on multivariate analysis of wheat genotypes into similar groups (clusters) and distinct color code (bullet graphs), respectively, we have been able to identify the relatively stable wheat genotypes in multi-environment trial across management practices. Results would tend to confirm the effectiveness of grouping and multivariate analysis in delineate groups which differed in performance and stability. Based on the available result, it is possible to breed stable genotypes with enhanced heat stress and quality traits. We propose that the productivity of adapted wheat genotype is more likely controlled by typical physiological processes related to sink development, source availability, temperature and solar radiation. While, productivity of an un-adapted wheat genotype is likely to be limited by timing of growth stages being inappropriate for the environment. Across locations, the genotype 'CSW 18' (G03), 'DPW 621-50' (G05), 'BAZ' (G01) were the best performer and high stable in early, normal and later sowing dates, respectively. Like across locations, BR shared more or less same pattern of predictive yield and grouping of stable genotypes across management practices. Thus, location specific stable genotypes across shifted sowing date is same for BR and across location. While, location MP and PB revealed zig-zag pattern of predictive yield across management practices. Similarly, stable genotypes varied for location MP and PB. Across and within an individual location (s), the pattern of predicted yield suggests that the low performing genotypes during early sowing dates tend to become high performer during late sowing dates (Fig. 3). Similarly, category 1 genotypes (high predictive yield and high stable) from early planting were qualified for category 2 (high predictive yield and low stable) or category 3 (low predictive yield and low stable) genotypes during normal and late sowing dates for across and within an individual location(s). Pedigree of category 3 genotypes from within an and across location(s) analysis confirmed the presence of heat stress, stem rust (*Sr2*, *Sr2+*, *Sr11+*), leaf rust (*Lr1*, *Lr10*, *Lr13*, *Lr13+*), yellow rust (*Yr2+*) and glutenin

(*Glu-A1b*, *Glu-B1b*, *Glu-D1a*) genes (Table 1). Glutenin (a type of gluten) is the major protein of wheat flour. These genotype include 'BAZ' (G01), 'GW 322' (G08), and 'PBW 550' (G21). Therefore, researchers can introgress genes from category 3 genotypes into elite inbreds to make better hybrids with high stability.

In conclusion, across locations, changes in date of sowing from Oct 15 to Dec 17 predicted to give high yield for early planted low performing genotypes. Similar pattern of yield prediction was noticed for individual location BR and MP. Divisive cluster analysis identified the representative and distinct genotypes, based on their yield performance, which breeders may consider to exploit their genetic diversity for future parents and developing multi-target breeding programs. These distinct genotypes ranged from high to low in performance and stability. Genotypes 'CSW-16' (G02); 'CSW-18' (G03) and 'HD-2967' (G14); and 'DPW-621-50' (G05) found to be distinct genotypes for across locations during early, normal and late date of sowing, respectively. Across dates of sowing, the number of divisive clusters of location BR and PB formed a funnel shape which suggest that performance of all wheat genotypes were equally affected with terminal heat stress whereas early planted genotype had differential response. In contrast, location MP revealed zig-zag pattern of number of clusters while 'Munal' (G19) and 'JW-3288' (G16) being consistently distinct and representative genotypes across all the date of sowing. This zig-zag pattern suggest that responded differently within early, normal and late date of sowing. Stability is likely to be highly affected by date of sowing and environmental conditions. The specific location analysis determined the magnitude of these effects. As shown previously that date of sowing affect the phenology and thereby development and adaptation (Lee et al., 2016). Across locations, we recommend genotypes 'CSW-18' (G03), 'DPW-521-50' (G05) and 'BAZ' (G01) are a promising option in terms of high predictive yield and stability for early, normal and late planting, respectively. Combined results of stability and yield performance across dates of sowing for individual location presented in bullet plots provide quick reference to growers to choose desired genotype. Further research is needed to explore the geospatial and temporal effects of meteorological parameters on wheat adaptation and yield across the IGP.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <https://doi.org/10.1016/j.fcr.2017.12.020>.

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